Amendments to the Specification:

Please replace paragraph **[0046]** with the following amended paragraph:

[0046] Figs. 2A to 2D show the alignment of PspCs (SEQ ID NOs: 1 to 13) (the amino acid sequences which include the α helical region and the proline-rich region of PspC were aligned using MacVector 6.0; the direct repeats within the α helix, the non-coiled-coil block, and the proline-rich region are indicated with arrows; conserved regions are shaded, and gaps are shown with a dash (-); taxons are named for the strain from which the gene was cloned with the exception of Genbank entrees: SpsA1 (Y10818) from strain ATCC33400 (serotype 1), SpsA2 (AJ002054) from strain ATCC11733 (serotype 2), SpsA47 (AJ002055) from strain NCTC10319 (serotype 47), CbpA (AF019904) from strain LM91 (serotype 2), C3bp (AF067128), and tigr from a serotype 4 clinical isolate ~~(http//:www.tigr.org)~~; the capsular serotypes of the other strains are as follows: EF6796 (6A), BG8090 (19), L81905 (4), DBL6A (6A), BG9163 (6B), D39 (2) and E134 (23));

Please replace paragraph **[0098]** with the following amended paragraph:

[0098] The sequences of *cbpA* and *spsA* both included sequences of D39 or its derivatives. Rosenow et al. sequenced *cbpA* from LM91 a *pspA*- mutant of D39 (Rosenow et al. 1997); and Hammerschmidt et al. sequenced *spsA* from an encapsulated derivative of R36A (ATCC11733) (Hammerschmidt et al. 1997; *see also* Figs. 8, 9, 10). From a comparison of these two sequences, it was apparent that *spsA* sequence contained a 480 bp deletion within the gene. Because of this discrepancy, Applicants also reported a sequence of *pspC* from a cloned *Hind*III-*Eco*RI chromosomal fragment of D39 that was determined prior to the *cbpA* and *spsA* sequence (Brooks-Walter et al. 1997; *see also* applications cited under Related Applications, *supra*). This sequence matched exactly that of *cbpA*. Other sequences that were used for sequence alignment comparisons included two *spsA* sequences from capsular serotype 1 and 47 strains (Hammerschmidt et al. 1997), and the *pspC/cbpA/spsA* sequence from the capsular serotype 4 strain sequenced in the TIGR genome project ~~(accessed by the internet at http://www.tigr.org)~~.

Please replace paragraph **[0102]** with the following amended paragraph:

[0102] Sequencing of *pspC* was completed using automated DNA sequencing (ABI 377, Applied Biosystems, Inc., Foster City, CA). Sequence analyses were performed using the University of Wisconsin Genetics Computer Group (GCG) programs (Devereux et al. 1984), MacVector 6.5 (Oxford Molecular), Sequencer 3.0 (GeneCodes, Inc.), and DNA Strider programs (Salser et al. 1993). Sequence similarities of *pspC* were determined using the NCBI BLAST. Coil structure predicted by the *pspC* sequence was analyzed using Matcher (Fischetti et al. 1993). The accession number by Genbank/EMBL for the nucleotide sequences of PspC are as follows: EF6796-U72655, DBL6A-AF068645, D39-AF068646, E134 -AF068647, BG8090-AF068648, L81905 - AF068649, BG9163 -AF068650, DBL6A - AF068645, D39 - AF068646, E134 - AF068647, BG8090 - AF068648, L81905 - AF068649, and BG9163 - AF068650; and each of these sequences and GenBank results from the accession numbers are hereby expressly incorporated herein by reference *(See also* Figs. 11 and 15-21). Preliminary sequence data was obtained from The Institute for Genomic Research website ~~at http://www.tigr.org~~.

Please replace paragraph **[0125]** with the following amended paragraph:

[0125] The protection-eliciting PspC immunogen contained the entire proline-rich region. The alpha-helical regions of PspA/WU2 and PspC/D39 have essentially no homology. However, the proline-rich region of PspC is repetitive and homologous with PspA. It was possible that antibody to this region was responsible for the cross-protection we observed. This hypothesis was supported by the observation that antibody elicited to PspC reacted with PspA fragments that contained the proline-rich region but not with those that lacked the proline-rich region in direct ELISAs. Antibodies elicited by PspC also cross-reacted with PspA on Western blots. The likelihood that the protective cross-reaction of PspC immune sera is mediated through PspA was further strengthened by the sequence data released by TIGR ~~(accessed by the internet at http://www.tigr.org)~~. Extensive searches of the largely completed genome failed to find other pneumococcal gene sequences with as high a similarity with the PspC sequence domains as the proline-rich region of PspA.